

"Success usually comes to those who are too busy to be looking for it"

CSIR NET – Life Science

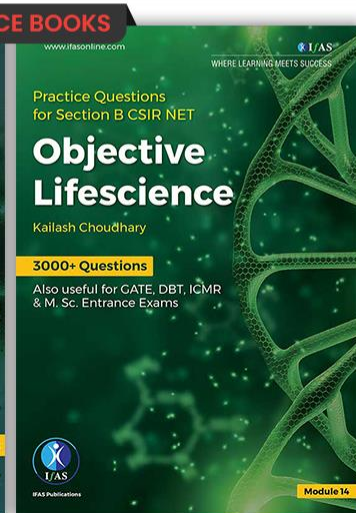
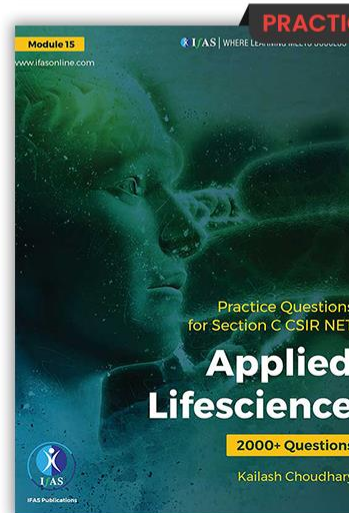
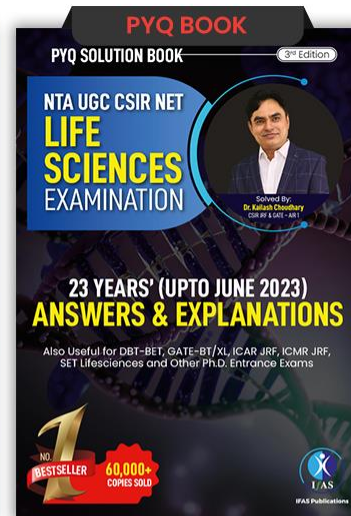
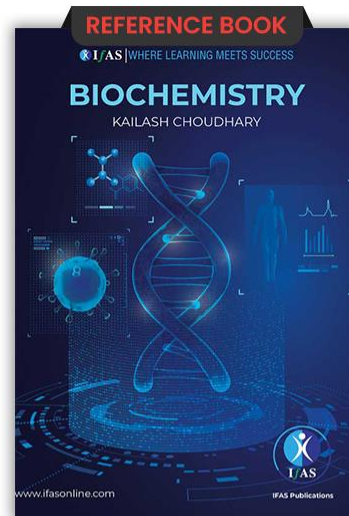
Unit 1: Biochemistry

11

Protein Stability & Kinetics









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Points to be covered in this Lecture

-  Protein folding
-  Stability and solubility of Protein
-  Rate of reaction
-  Order of reaction
-  What are Biocatalyst
-  Factors affecting enzyme activity





How do protein fold perfectly each time?



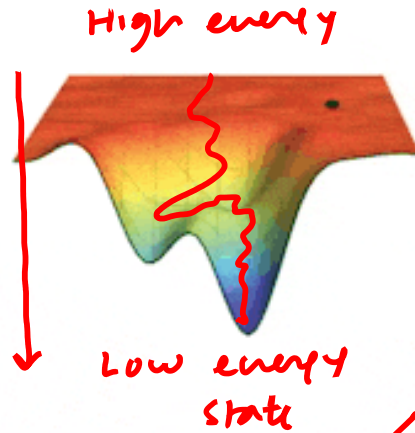
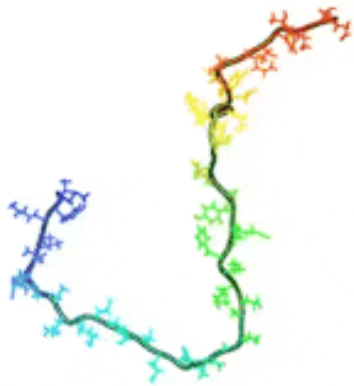
Driving force: Hydrophobic Interactions

During folding hydrophobic amino acids tend to move towards the inside of the protein structure, away from the aqueous cellular environment, while hydrophilic residues are more likely to be exposed on the surface.

Decrease in entropy of protein (solute)
Increase in entropy of water (solvent)

Increase in entropy of solution

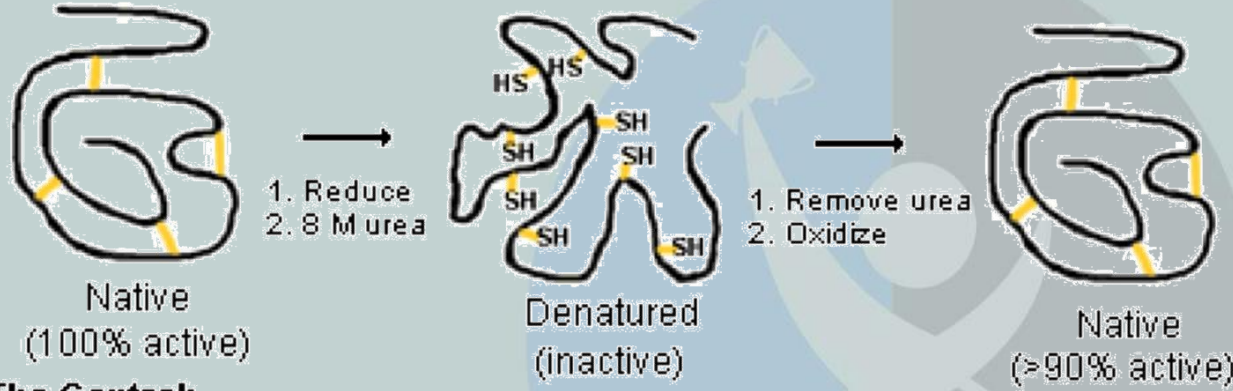
✓ Protein always adopt form which has least free energy



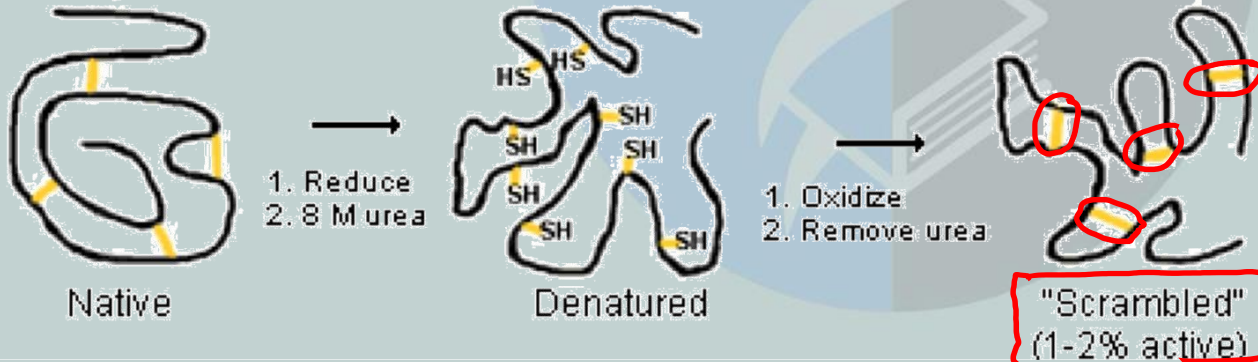
✓ Reversible Denaturation of Ribonuclease A: Christian Anfinsen

(RNase A)

The Observation:



The Control:



(1) Protein fold
(2) disulphide bonds may form.

Trace of β -me



Levinthal's paradox



If a protein with 100 amino acids, it would have 99 peptide bonds and 198 considerations for ϕ and ψ angles.

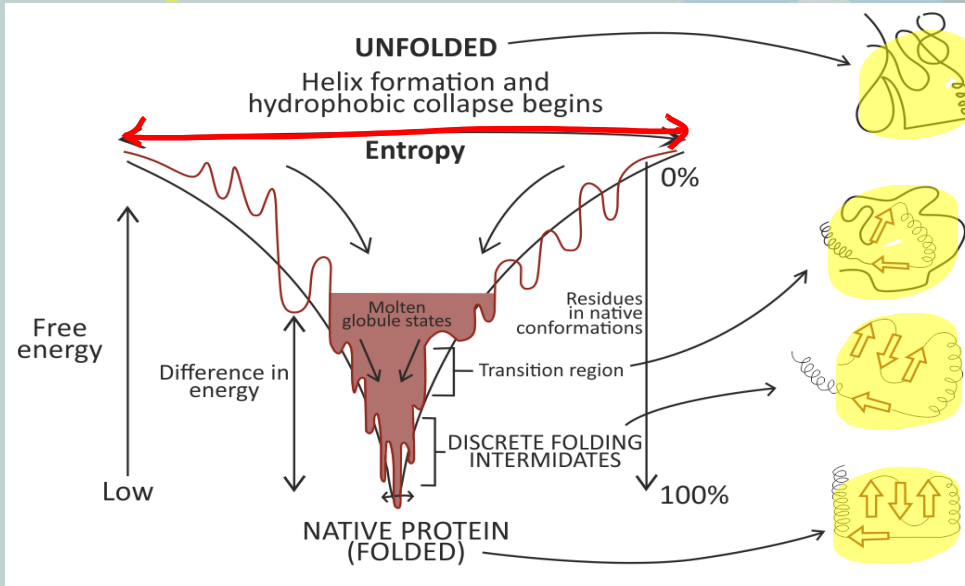
If each of these had only three conformations, that would result in 3^{198} different possible folding.

$$3 \times 3 \times 3 \dots = \boxed{\dots}$$

Levinthal suggested, proteins must fold by some sort of ordered pathway or set of pathways in which the approach to the native state is accompanied by sharply increasing conformational stability (decreasing free energy).

Energy Landscape Theory (Folding Funnel):

Polypeptides fold via a series of conformational adjustments that reduce their free energy and entropy until the native state is reached



• unfolded (molten globule)
many 2° str & no 3° str
Free energy = ↑, H = ↑, S = ↑

↓
↓ Intermediate states
↓

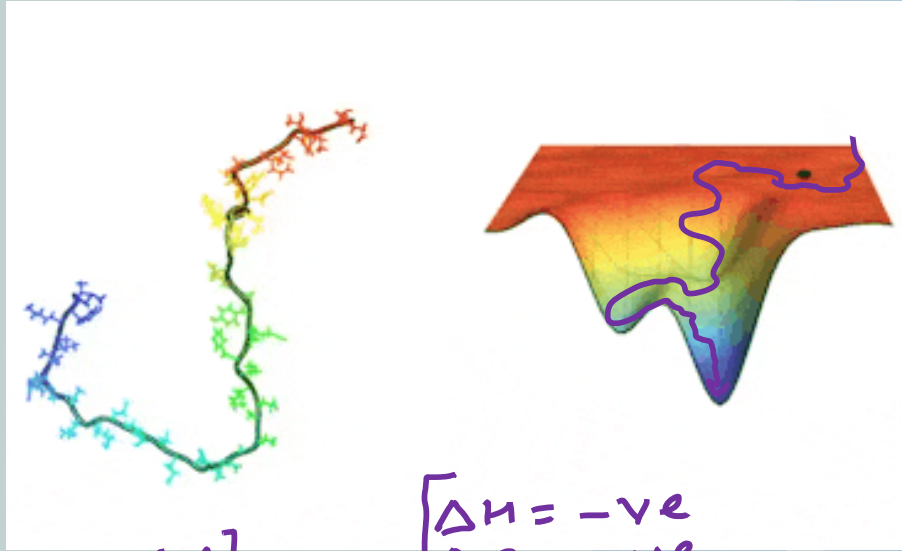
$$\begin{matrix} \Delta G = -ve \\ \Delta H = -ve \\ \Delta S = -ve \end{matrix} \quad T < \frac{\Delta H}{\Delta S}$$

Native folded state (3°)
G = ↓
H = ↓
S = ↓

water entropy = ↑

Single largest contribution to the stability of a folded protein is ΔS (solvent) for the nonpolar residues.

Thermodynamics of protein folding



$$T_m = \frac{\Delta H}{\Delta S}$$

$$\begin{cases} \Delta H = -ve \\ \Delta S = -ve \\ \Delta G = -ve \end{cases} \quad T < \frac{\Delta H}{\Delta S}$$

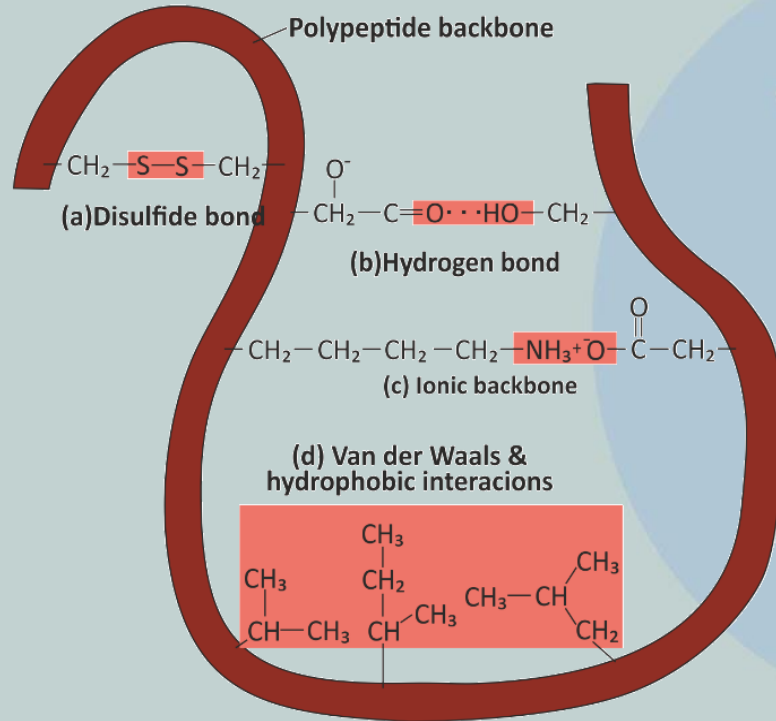
$$\Delta G^\circ = \Delta H^\circ - T \Delta S^\circ$$

$$\Delta G^\circ = -2.303 RT \log K_{eq}$$

$$UF \rightleftharpoons \text{folded}$$

$$K_{eq} = \frac{[F]}{[UF]}$$

PROTEIN STABILITY



- ✓ **Primary Structure:** Covalent bonds (*Peptide bond*)
- ✓ **Secondary structure:** Hydrogen bonds
- ✓ **Tertiary structure:** Hydrophobic interactions

3D structure is stabilized by

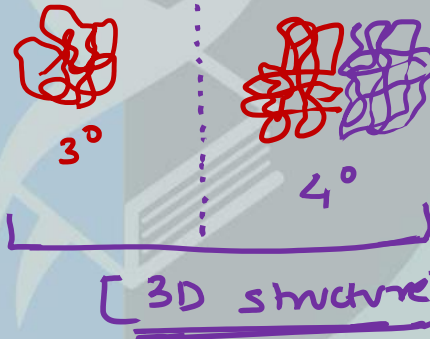
- Non-covalent interactions
- Disulphide bonds

Hydrophobic

hydrogen bond

electrostatic

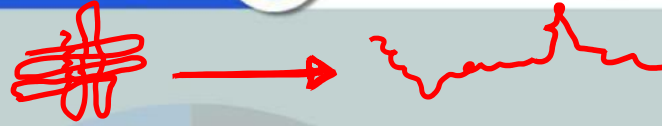
van der Waals



- X-Ray crystallography
- 2D-NMR spectroscopy
- Cryo electron microscopy



Conditions for denaturation



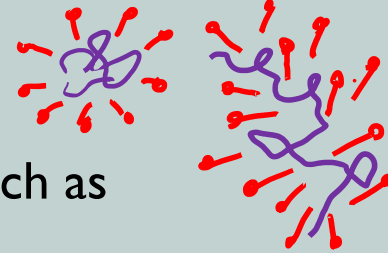
✓ pH variations: alter the ionization states of amino acid side chain

$pH = \downarrow$ $pH = \uparrow$

Asp, Glu
Lys, Arg
His

✓ Detergents: hydrophobically associate with the nonpolar residues

↳ SDS (-), CTAB (+), Triton-X (uncharged)



High concentrations of water-soluble organic substances such as aliphatic alcohols interfere with the hydrophobic forces

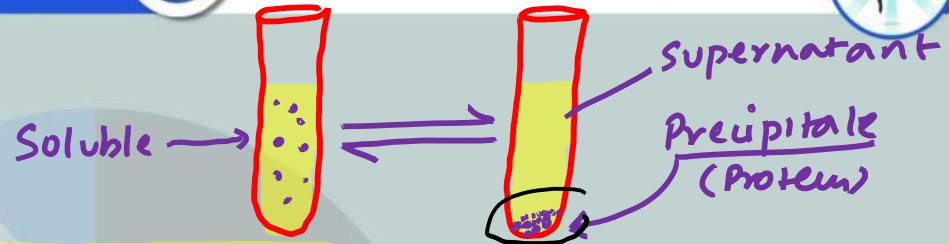
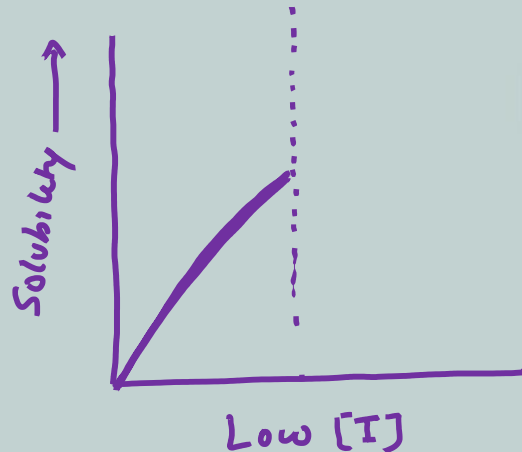
- Acetone ↑
- Butanol ↑
- Petroleum ether ↑



SOLUBILITIES OF PROTEINS

A. Effects of Salt Concentrations

Salting in: The solubility of a protein at **low ionic strength** generally increases with the salt concentration

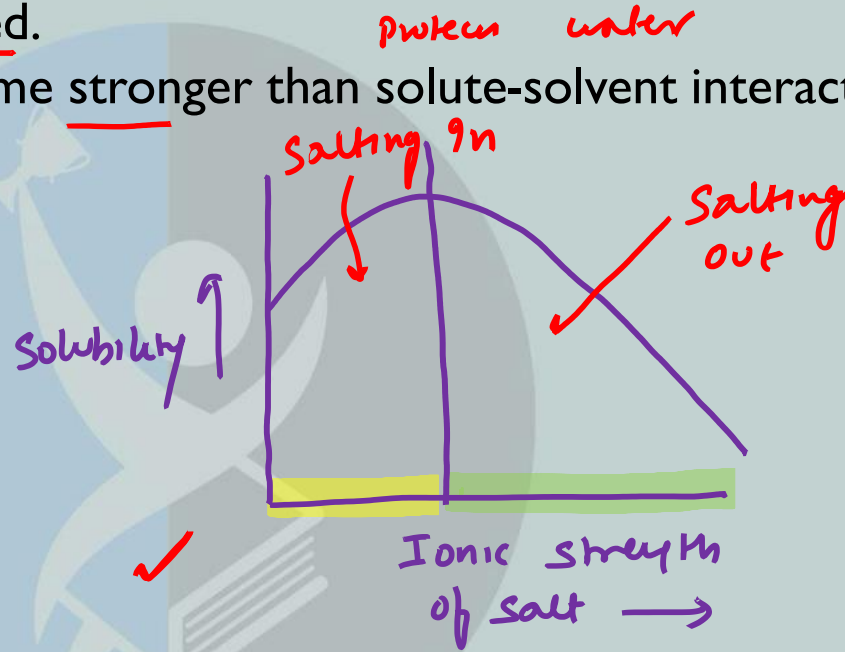
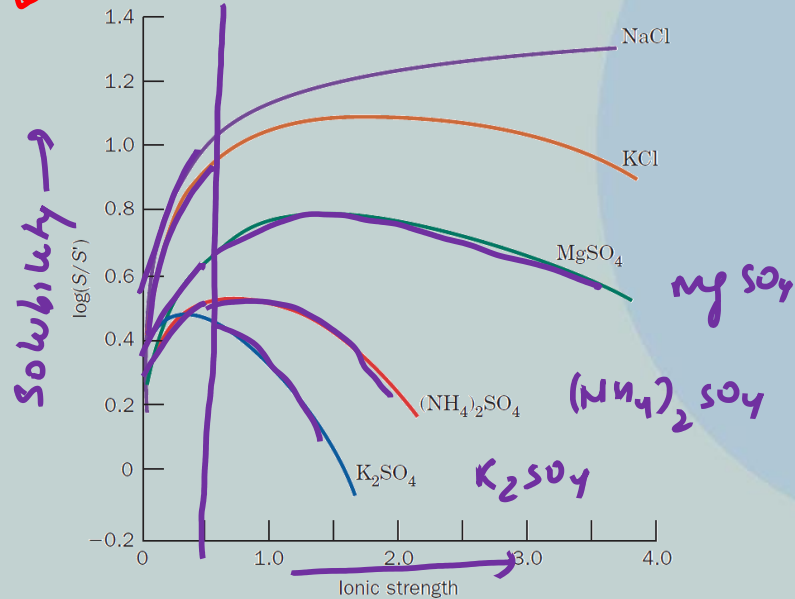


$$I = \frac{1}{2} \sum c_n \cdot z_n^2$$



Salting out:

- The solvent's activity is decreased.
- Solute-solute interactions become stronger than solute-solvent interactions and the solute precipitates.
protein - protein
- ✓ Ammonium sulfate





B. Effects of pH

Iso-electric precipitation: Solubility is minimum when surrounding pH is equal to pI of protein

$$pH = pI$$

$$pH < pI$$

$$pH > pI$$

Charge

0

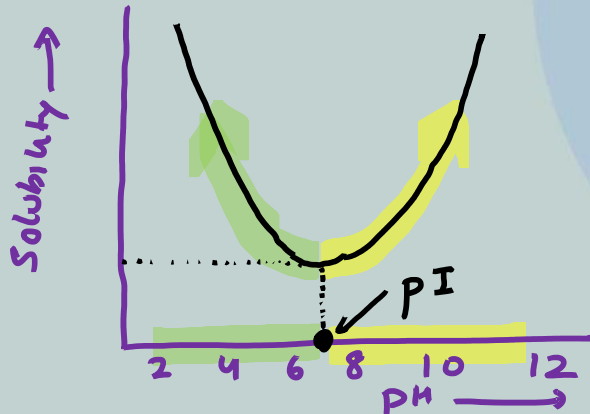
+

-

Solubility
minimum

↑

↑





C. Effects of Organic Solvents

✓ **Precipitant:** Low dielectric constant

Acetone and ethanol ✓

✓ **Solvent:** High dielectric constant

Dimethyl sulfoxide (DMSO) or N,N-dimethylformamide (DMF)

Glycerol

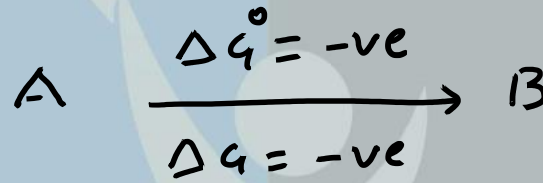
→ Hydration of protein
→ solubility = ↑





Chemical Kinetics

Spontaneous



- Standard conditions
- Physiological conditions

Rate = ? No idea

fast or slow

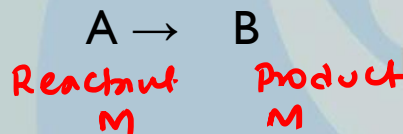
'Kinetics'



Reaction Kinetics

I. Rate of a Reaction or speed or velocity

It is defined as the change in concentration of a reactant or product per unit time. It is usually expressed in terms of molarity per second (M/s).



$$\text{Rate} = \frac{-\Delta[\text{A}]}{\Delta t} = \frac{\Delta[\text{B}]}{\Delta t}$$

$\leftarrow \frac{\text{M}}{\text{Sec}}$

$$\text{M} = \frac{\text{mol}}{\text{L}}$$

$$\underline{\text{M}} \text{ sec}^{-1}$$

$$\text{mol l}^{-1} \text{ sec}^{-1}$$



Factors affecting Rate of a Reaction

1. Concentration of Reactants:

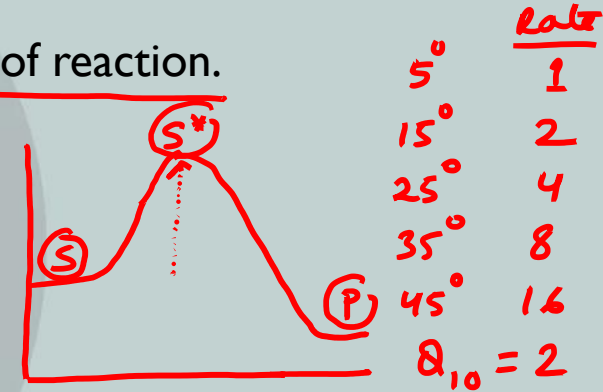
Increasing the concentration of reactants increases the rate of reaction.



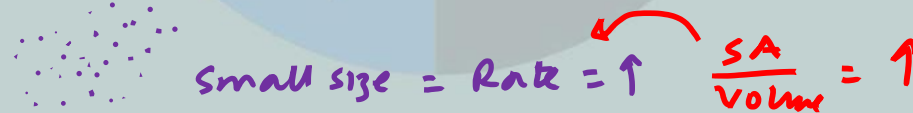
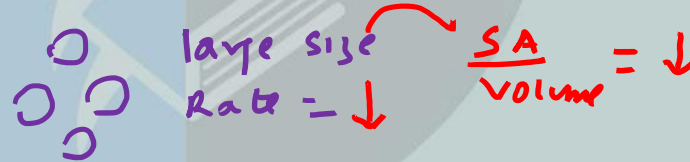
2. Temperature

$Q_{10} = 2$ Rate doubles with change of every 10°C

Increase in temperature increases the rate of reaction.

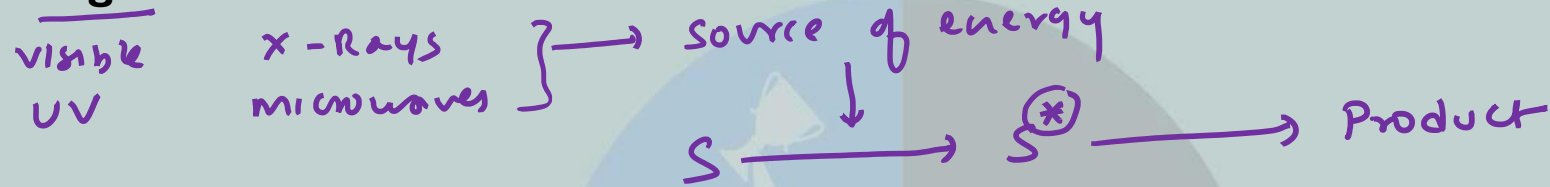


3. Surface Area of Reactants:

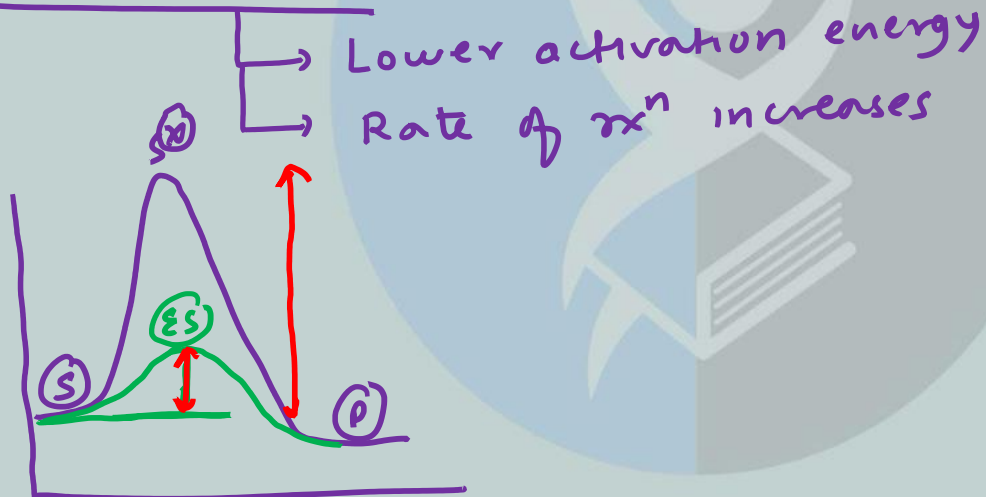




4. Light /Radiations:



5. Presence of a Catalyst:





2. Molecularity of a reaction

Number of molecules reacting in an elementary step.





3. Order of reaction:

How the reaction rate is influenced by the **concentration of the reactants** under a given set of conditions.

It is sum of the powers to which all reactant concentrations are raised in the rate law equation.



$$\begin{aligned} \text{rate} &\propto [\text{A}]^m [\text{B}]^n \\ \text{rate} &= K [\text{A}]^m [\text{B}]^n \end{aligned}$$

The rate law for a reaction can be expressed generally as $\text{rate} = k[\text{A}]^m[\text{B}]^n$

• m and n are the **orders of the reaction** with respect to **reactants A** and **B**, respectively. The overall order of the reaction is $m+n$



First order reaction:

- The **rate of reaction** is directly proportional to the concentration of **one reactant**.
- A common example is **radioactive decay**.



$$\frac{dc}{dt} \propto -[A] = [P]$$

$$\frac{dc}{dt} = -\textcircled{K}[A] = K[P]$$

Unit of first order rate constant:

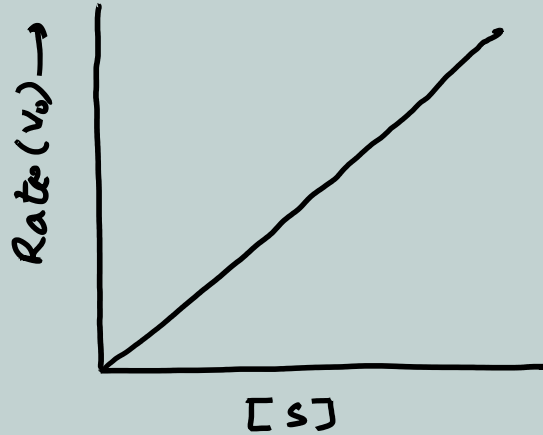
$$\frac{M}{s} = \textcircled{K} \cdot M$$

$$K = \frac{M}{s} \cdot \frac{1}{M}$$

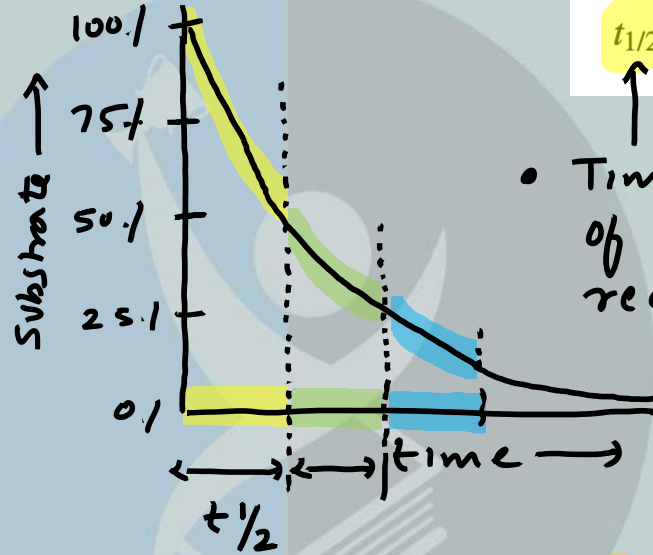
$$K = 1/s = s^{-1} \text{ (sec}^{-1}\text{)}$$



Rate v/s Substrate



Concentration v/s time

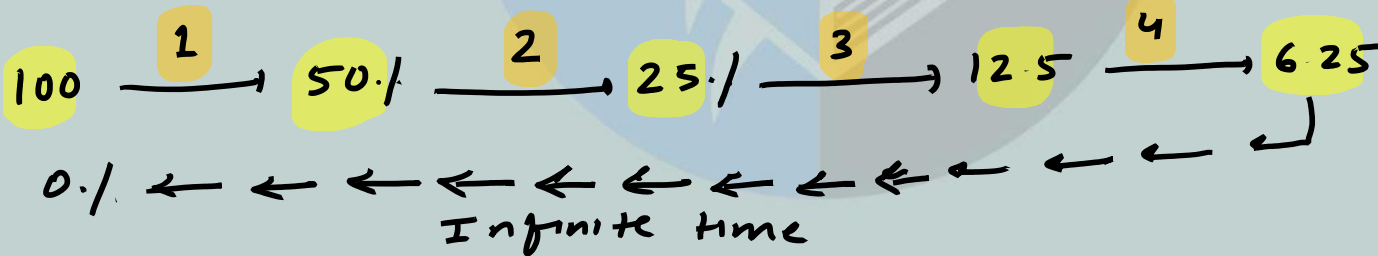


$$t_{1/2} = \frac{\ln 2}{k} \approx \frac{0.693}{k}$$

- Time in which concⁿ of original substrate reduces to half

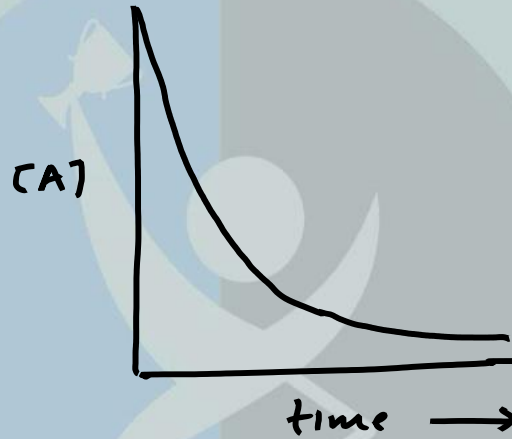
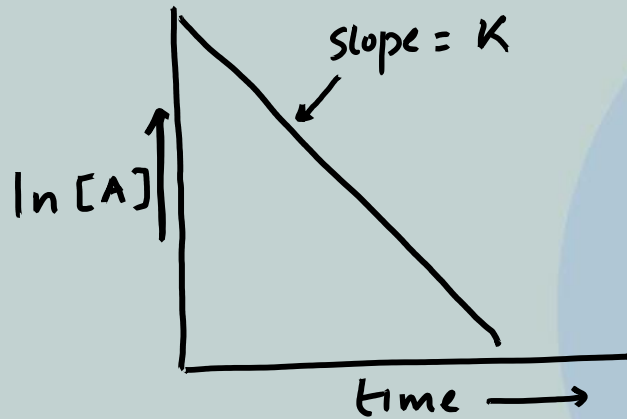
- $T_{1/2}$ is constant

$$T_{1/2} \propto \frac{1}{k} \quad T_{1/2} = \frac{\ln 2}{k}$$





For straight line plot $\ln[A]$ with time





Apply your mind:

If half life of Radioisotope is 10 min, what would be the concentration of radio isotope left after 30 minutes?

✓ (1) 12.5 %

(2) 25 %

(3) 50 %

(4) 75 %

$$\frac{30 \text{ min}}{10 \text{ min}} = 3 \leftarrow \text{Half life.}$$

$$100 \xrightarrow{1} 50 \xrightarrow{2} 25 \xrightarrow{3} 12.5 \text{ left}$$

Decay 0	50 %	75 %	87.5 %
100 - 100	100 - 50	100 - 25	100 - 12.5
= 0	= 50	= 75	= 87.5



Apply your mind:

If half life of radioisotope is 1 day, in what duration its concentration will reach to zero?

- (1) 1 min
- (2) 1 day
- (3) 1 year
- ✓ ~~(4)~~ Infinite

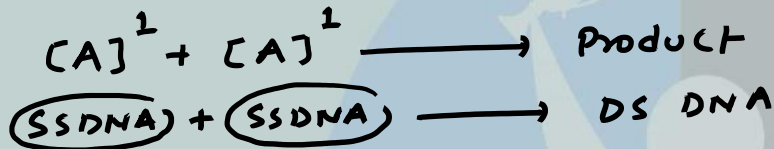




Second order reaction:

[S]	1	2	3	4	5	6	
V_0	1	4	9	16	25	36	← Second order

The rate of reaction is proportional to the square of the concentration of one reactant



$$\frac{dC}{dt} = K [A]^1 [B]^1$$

order = 1 + 1 = 2

$$\frac{dC}{dt} \propto [A]^2$$

$$\frac{dC}{dt} = K \cdot [A]^2$$

order = 2

$$\frac{\text{mole}^{-1}}{\text{lt}} \frac{\text{lt}}{\text{sec}^{-1}}$$

Unit of second order rate constant:

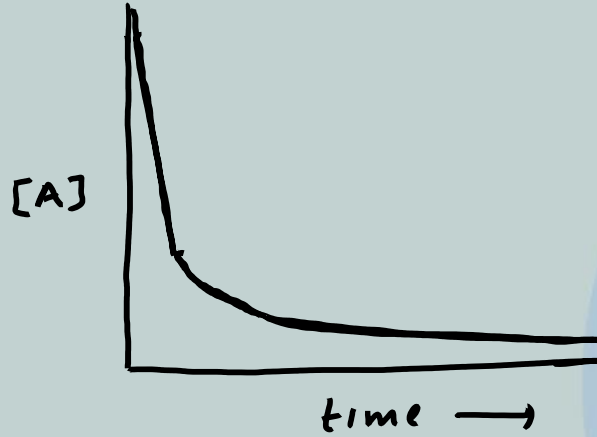
$$\frac{M}{\text{Sec}} = K \cdot M \cdot M$$

$$K = \frac{M}{\text{sec}} \cdot \frac{1}{M} \cdot \frac{1}{M}$$

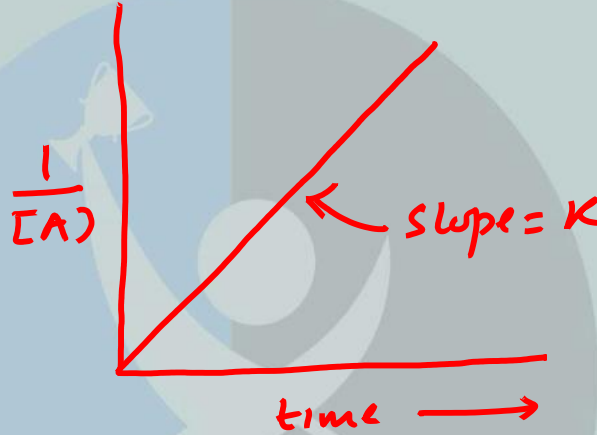
$$K = \frac{1}{M} \cdot \frac{1}{\text{sec}} \propto M^{-1} \text{sec}^{-1}$$



Concentration v/s time



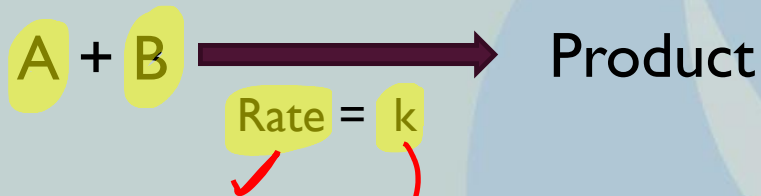
For straight line plot $1/[A]$ with time





Zero order reaction:

The rate **does not vary** with the **increase or decrease** in the concentration of the reactants



- I order : sec^{-1}
- II order : $\text{M}^{-1} \text{sec}^{-1}$
- Zero order : $\text{M}^1 \text{sec}^{-1}$

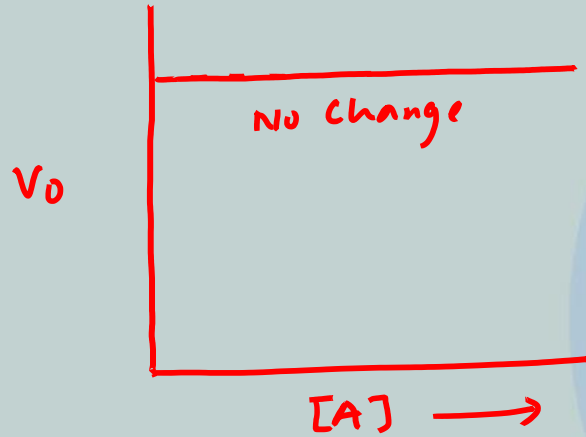
[K]
(Imp)

Unit of zero order rate constant:

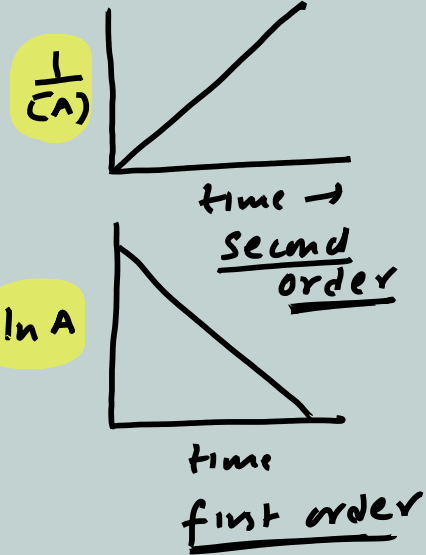
$$\frac{\text{M}}{\text{sec}} = \text{M}^1 \text{sec}^{-1}$$



Velocity versus substrate



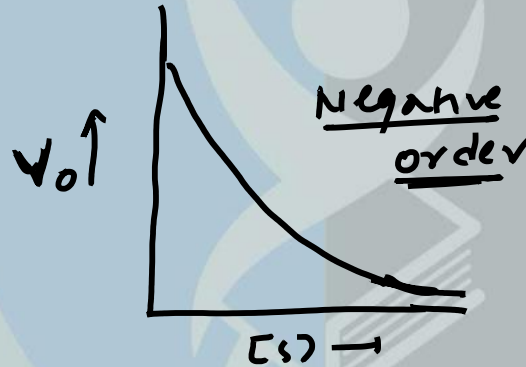
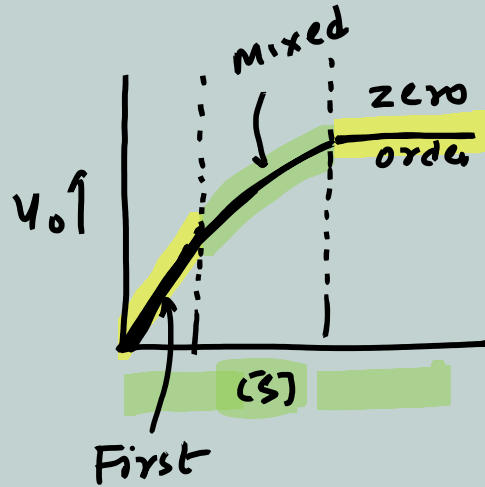
Concentration versus time





Fractional (mixed order) and Negative Orders:

Sometimes, the order of a reaction with respect to a reactant can be fractional or even negative, depending on the reaction mechanism.



v_0 = observed velocity



Enzymes

Bio - catalyst

in - yeast

catalyst

Accelerate
rate of reaction

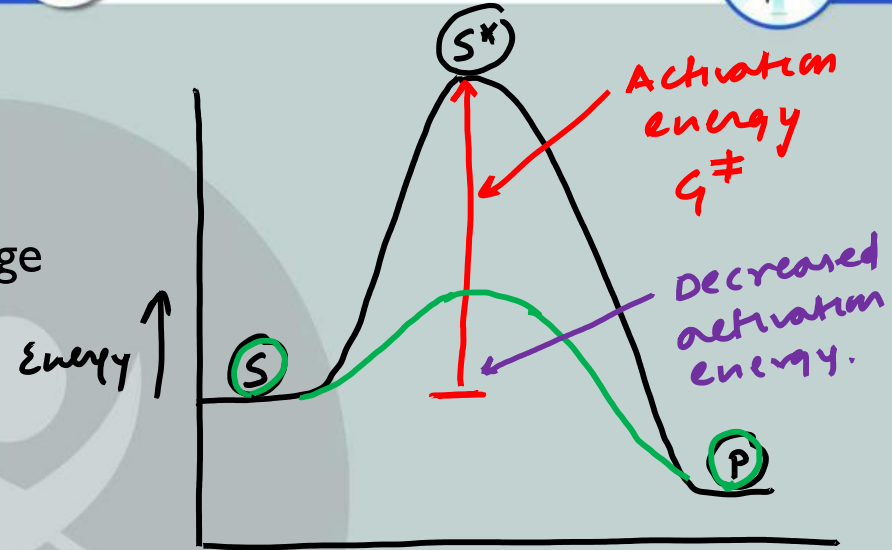


What are catalyst?

- ✓ Participate in reaction
- ✓ Not consumed or any permanent change
- ✓ Required in very small quantities.
- ✓ Lowers the activation energy
- ✓ Enhance the rate of reactions
 - Do not change the equilibrium.
 - Do not influence free energy change.

$$\Delta G^\circ = -2.303 RT \log (K_{eq})$$

- catalyst donot decide direction of reaction
- Allow equilibrium to get achieved in small time.



$$\Delta G = -ve$$

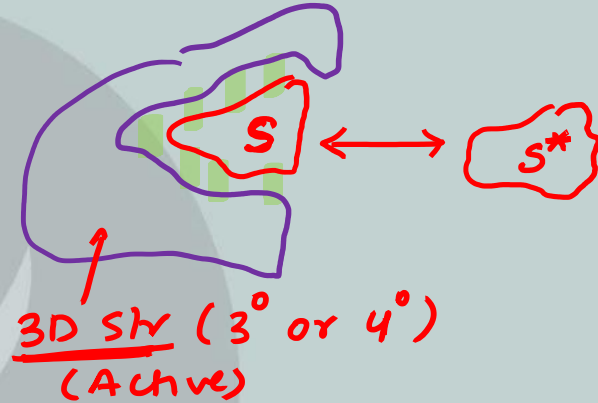
(No change)



Enzymes/Biocatalyst: Organic in nature

99.1% less than 1.0%

- Proteins or RNA
- Substrate specific, stereo-specific
- Enhance rate of reaction by forming weak interactions with substrates.
- Work at optimum pH and temperature



Active site of enzyme

The active site is a 3-D cleft formed by R-groups of amino acids that come from different parts of the amino acid sequence.

The active site takes up a relatively small part of the total volume of an enzyme.

• at least 100 aa

Framework



Active site

Active site

- Substrate(s) binding site
- Co-factor(s) binding site
- Catalytic site.

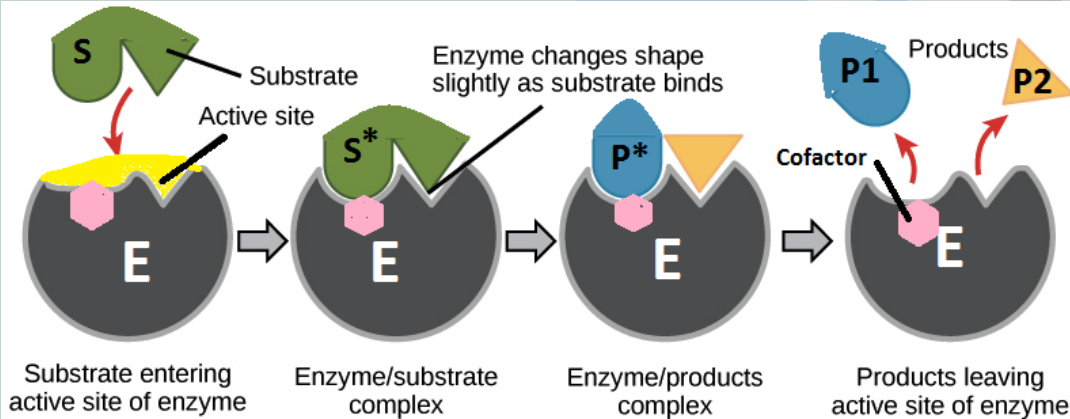
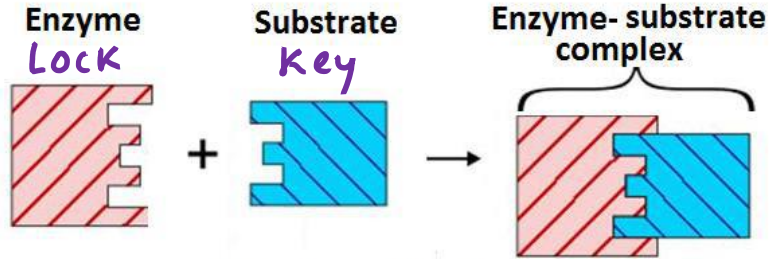


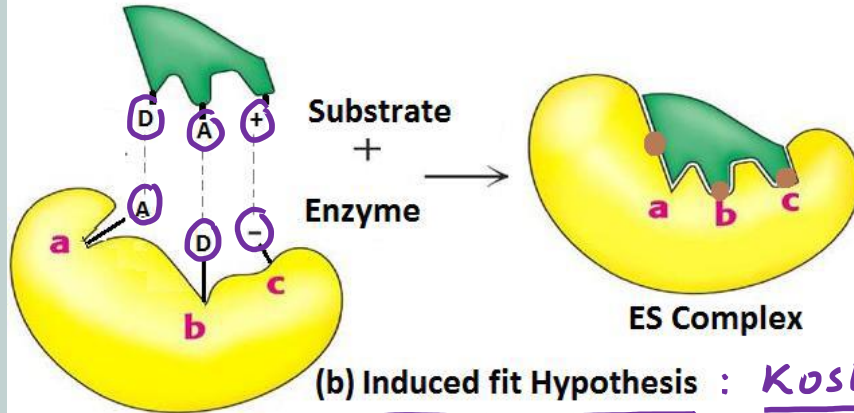
Figure 3: Active site of Enzyme and Enzyme catalysis

More than 100 aa

Enzyme Specificity



(a) Lock and Key Hypothesis : Fischer



(b) Induced fit Hypothesis : Koshland

Figure 3: Interaction between enzyme and substrate

Non-covalent Interactions between enzyme and substrate

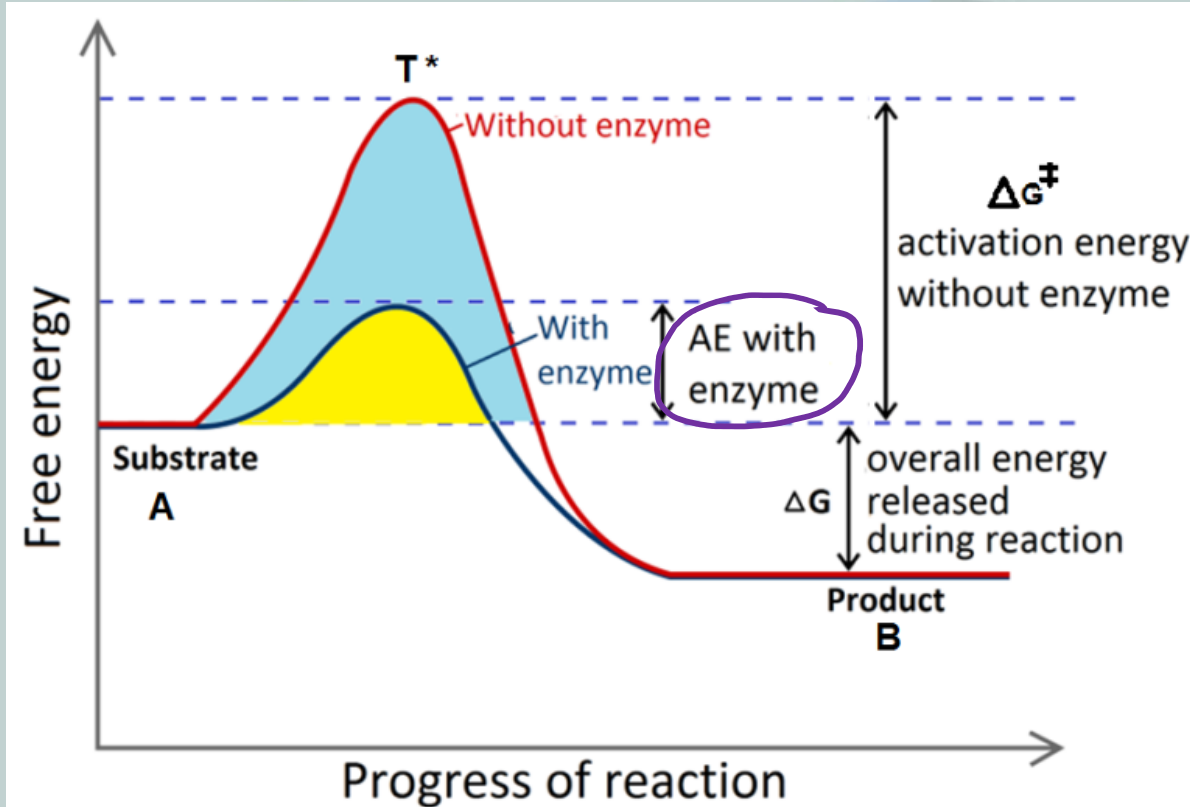
Specific

Induces conformational change such that substrate can get fit into it.

← structural compatibility

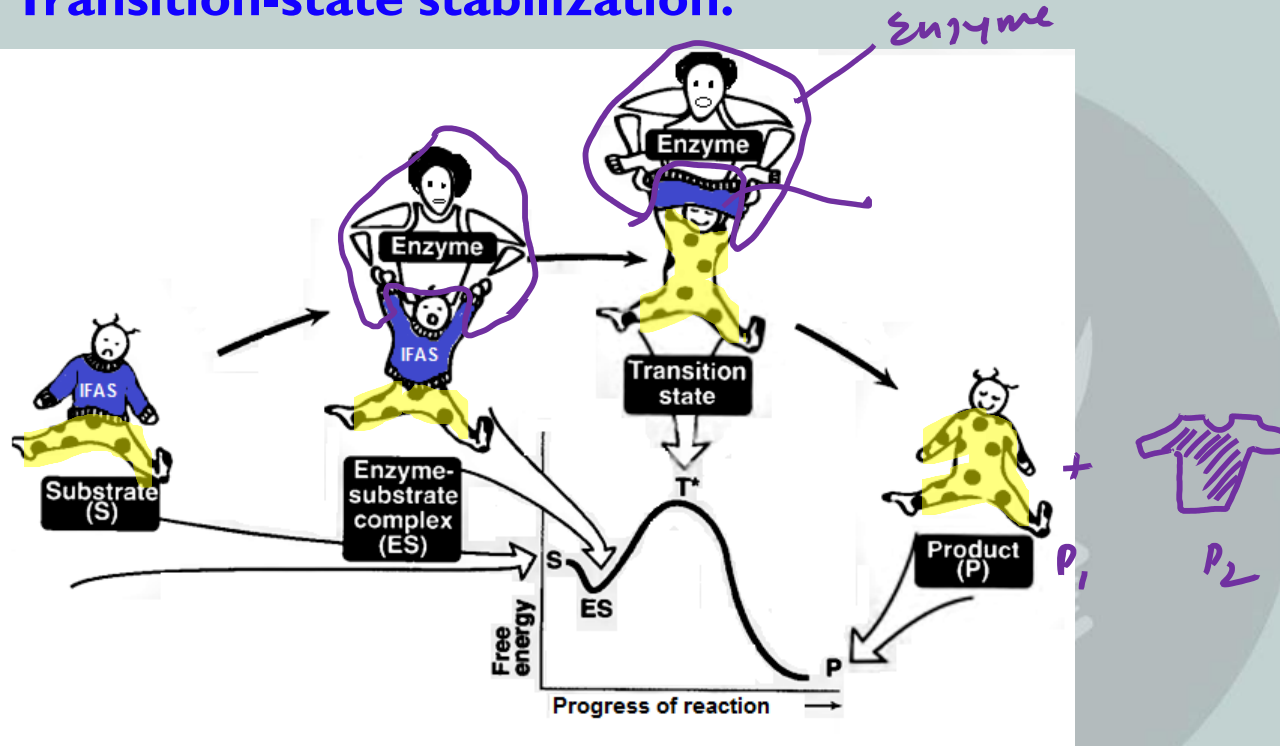


Free energy of activation



- Enzyme provide alternative pathway for reaction completion
- needs lesser activation energy
- Rate increases

Transition-state stabilization:

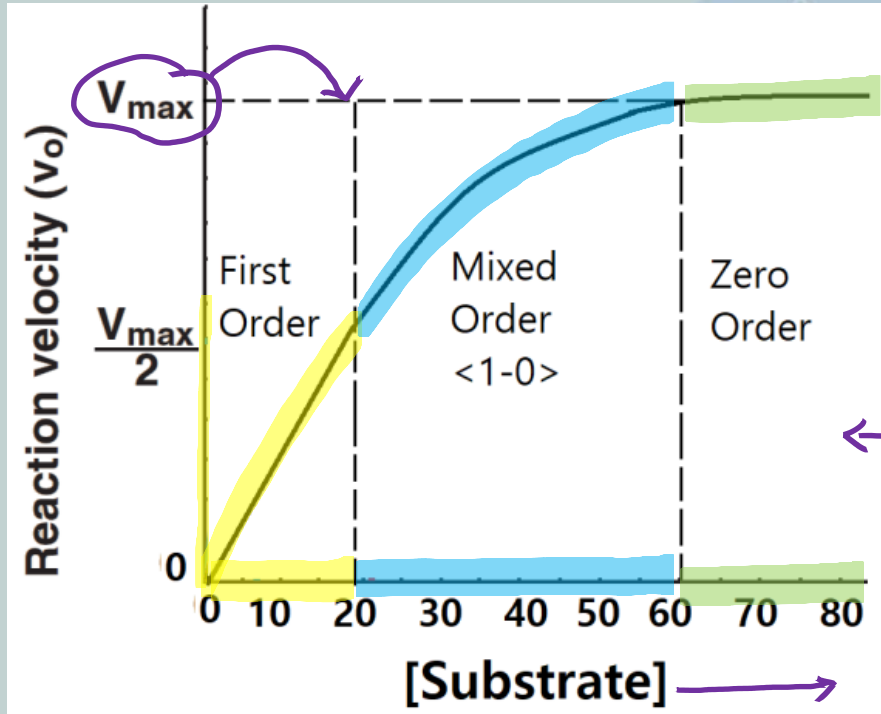


Binding energy due to multiple weak interactions with substrate, decreases activation energy required to achieve transition state



FACTORS AFFECTING REACTION VELOCITY

A. Substrate concentration



low $[S]$ = First order

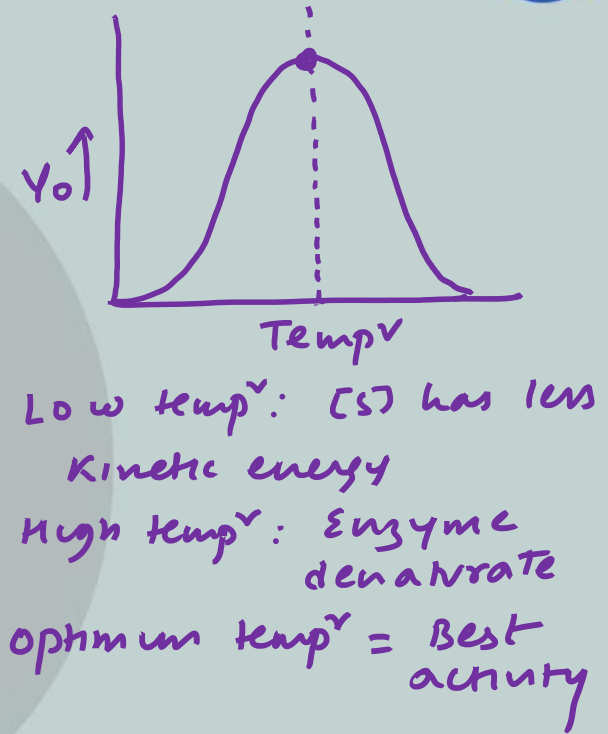
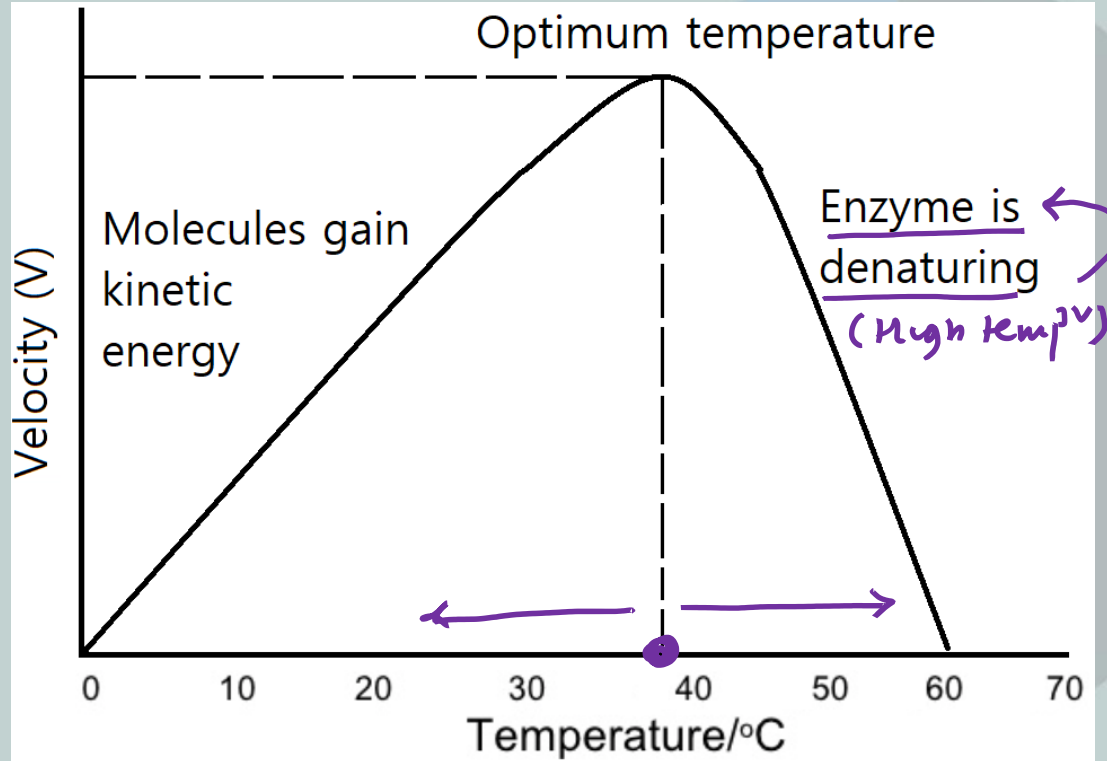
Very high $[S]$ = Zero order

Intermediate $[S]$ conc^y
= mixed order
= $\langle 1 - 0 \rangle$

← Rectangular
Hyperbolic
curve.

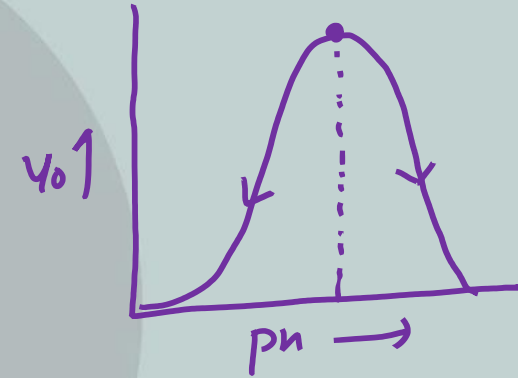
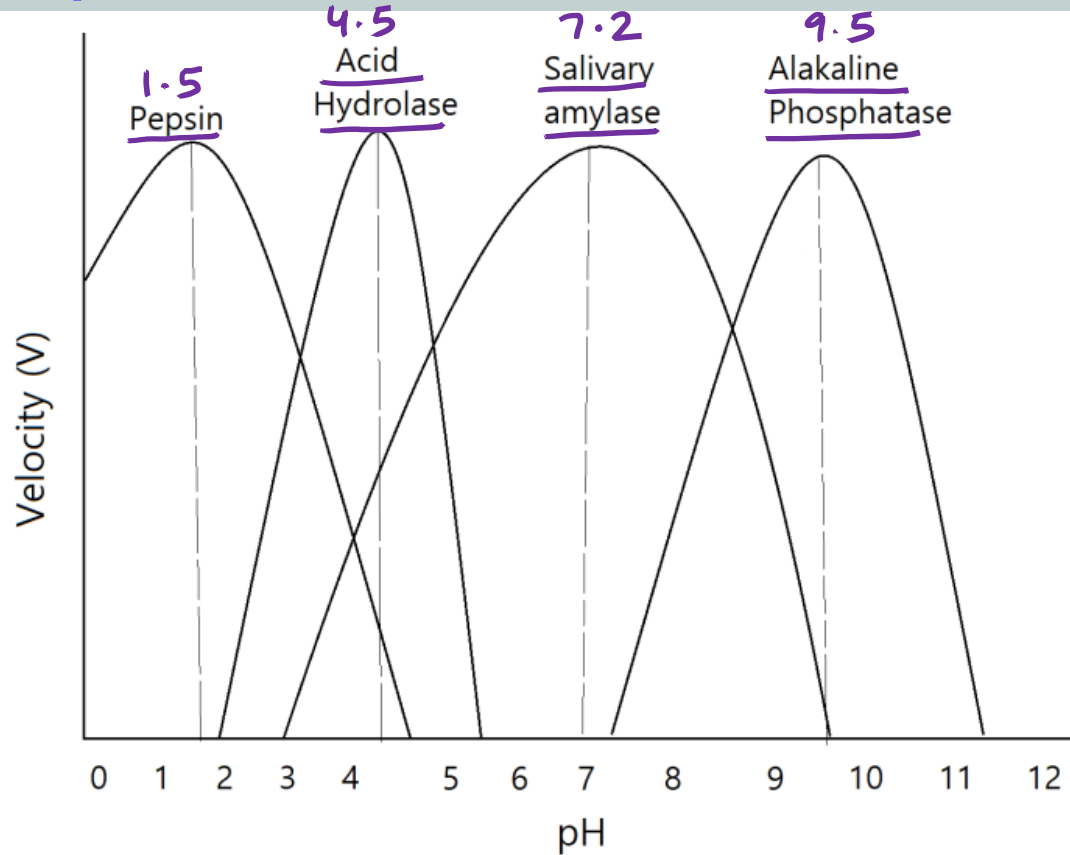


B. Temperature





C. pH → change in ionization state of protein which may alter active conformation





Enzyme Classes: International Union of Biochemistry and Molecular Biology (IUMB)

Group	Class of enzyme	Reaction carried out	OTHLILigase 1 2 3 4 5 6	Example
1	Oxidoreductases	Transfer of electrons	$A^- + B \longrightarrow \underline{A} + \underline{B^-}$	Alcohol dehydrogenase Oxidase, Reductase
2	<u>Transferases</u>	Transfer of <u>C-</u> , <u>N-</u> or <u>P-containing</u> groups	$A-\underline{B} + C \longrightarrow A + \underline{B-C}$	<u>Hexokinase</u> (Phosphate)
3	<u>Hydrolases</u>	<u>Bond cleavage</u> by <u>addition</u> of <u>water</u>	$A-B + \underline{H_2O} \longrightarrow A-\underline{H} + B-\underline{OH}$	Trypsin Digestive enzyme
4	<u>Lyases</u> (Synthase)	Cleavage of C-C, C-S and C-N bonds often to form a double bond	$\begin{array}{c} A-B \\ \quad \\ C \quad D \end{array} \longleftrightarrow \underline{A=B} + \underline{C-D}$	Pyruvate decarboxylase RUBISCO Citrate lyase, Aldolase malate synthase
5	<u>Isomerases</u>	Formation of <u>optical</u> or <u>geometric</u> isomers	$\begin{array}{c} A-B \\ \quad \\ C \quad D \end{array} \longrightarrow \begin{array}{c} A-B \\ \quad \\ D \quad C \end{array}$	<ul style="list-style-type: none"> Maleate isomerase Epimerase Racemase Mutase
6	<u>Ligases</u> (Synthetase)	Hydrolysis of high energy phosphates to form new bonds.	$\underline{A} + \underline{B} \xrightarrow[\text{GTP}]{\text{ATP}} \underline{A-B}$ ATP → ADP GTP → GDP	<ul style="list-style-type: none"> Pyruvate carboxylase DNA ligase

Cofactor

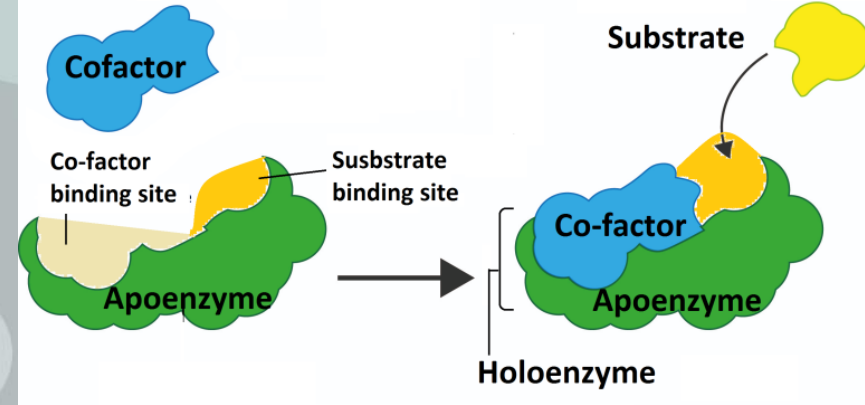
Inorganic
Metals

Organic
Co-enzymes

Nm-covalent →
Weak binding

Strong binding
Prosthetic group

← *Covalent*





Inorganic Co-factors

Zn^{2+}	Carbonic anhydrase Carboxypeptidase Alcohol dehydrogenase
Mg^{2+} Mg^{2+}	Restriction endonuclease DNA/RNA polymerase Hexokinase
Ni^{2+}	Urease
Mo	Nitrate reductase Nitrogenase
Se	Glutathione peroxidase
Mn^{2+}	Superoxide dismutase Water splitting enzyme (PSII) Arginase
K^+	Propionyl CoA carboxylase
Cu^{2+}	Tyrosinase Uric acid oxidase Ascorbic acid oxidase Cytochrome oxidase
Fe^{2+}	Cytochrome Catalase Hydrogenase Nitrogenase

Divalent metal ions

mg^{2+} , ca^{2+} , Fe^{2+} , Co^{2+} , Zn^{2+} , Mo^{2+} , Mn^{2+}

K^+ : Pyruvate kinase

monovalent Propionyl CoA carboxylase



Co-enzyme: carriers of specific chemical groups, mostly derived from water soluble vitamins (B & C)

Organic co-factor		
Thiamine pyrophosphate B_1 ✓	Transketolase Pyruvate dehydrogenase	← C-C cleavage & formation rx ⁿ
Flavin mono nucleotide (FMN) } B_2	NADH dehydrogenase	} electron transfer (oxd-red)
Flavin adenine nucleotide (FAD) }	Succinate dehydrogenase	
Nicotinamide adenine dinucleotide (NAD) B_3	Lactate dehydrogenase	} electron transfer (oxd-red)
Pyridoxal phosphate (PLP) B_6 ✓	Glycogen phosphorylase Amino transferase	← Amino group transfer
Coenzyme A (CoA) B_5	Acetyl CoA carboxylase	← Acyl group transfer
Biotin B_7	Pyruvate carboxylase	← carboxylation rx ⁿ
5'-Deoxyadenosyl cobalamin B_{12}	Methylmalonyl mutase	← methyl group (1C) transfer
Tetrahydrofolate (THF) B_9	Thymidylate synthase	← 1C, methyl or formyl group transfer
Ascorbic acid C	Prolyl hydroxylase	← OH group transfer
Menaquinone (vit K)	γ - Carboxylase	← CO ₂ transfer
S-adenosyl methionine (SAM) B_6	DNA methyl transferase	← methyl transfer
Glutathione .E-C-G	Glutathione peroxidase	← oxidation rx ⁿ .
Lipoamide	Pyruvate dehydrogenase	
Heme	Cytochrome, Catalase	



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